

EXHIBIT 6



AGC GGC TGG GAG GGC CGC TTC TGC CAG CGC GGTGAGGGGG AGAGGTGGAT Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg 91	3236
GCTGGCGGGC GGCGGGGCGG GGCTGGGGCC GGGTTGGGGG CGCGGCACCA GCACCAGCTG CCCGCGCCCT CCCCTGCCCC CA GAG GTG AGC TTC CTC AAT TGC TCT CTG GAC Glu Val Ser Phe Leu Asn Cys Ser Leu Asp 92	3296 3348
AAC GGC GGC TGC ACG CAT TAC TGC CTA GAG GAG GTG GGC TGG CGG CGC Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg	3396
TGT AGC TGT GCG CCT GGC TAC AAG CTG GGG GAC GAC CTC CTG CAG TGT Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys	3444
CAC CCC GCA GGTGAGAAGC CCCCAATACA TCGCCAGGA ATCACGCTGG His Pro Ala 136	3493
GTGCGGGGTG GGCAGGCCCC TGACGGGCGC GGC GCGGGGG GCTCAGGAGG GTTCTAGGG	3553
AGGGAGCGAG GAACAGAGTT GAGCCTTGGG GCAGCGGCAG ACGCGCCCAA CACCGGGGCC	3613
ACTGTTAGCG CAATCAGCCC GGGAGCTGGG CGCGCCCTCC GCTTTCCTG CTTCCTTTCT	3673
TCCTGGCGTC CCCGCTTCT CCGGGCGCCC CTGCGACCTG GGGCCACCTC CTGGAGCGCA	3733
AGCCCAAGTG TGGCTCCGCT CCCAGTCTG AGCGTATCTG GGGCGAGGCG TGCAGCGTCC	3793
TCCTCCATGT AGCCTGGCTG CGTTTTTCTC TGACGTTGTC CGGCGTGCAT CGCATTTCCC	3853
TCTTTACCCC CTTGCTTCT TGAGGAGAGA ACAGAATCCC GATTCTGCCT TCTTCTATAT	3913
TTTCCTTTTT ATGCATTTTA ATCAAATTTA TATATGTATG AAACTTTAAA AATCAGAGTT	3973
TTACAACTCT TACACTTTCA GCATGCTGTT CCTTGGCATG GGTCTTTTT TCATTCAATT	4033
TCATAAAAGG TGGACCCCTT TAATGTGGAA ATTCCTATCT TCTGCCTCTA GGGCATTAT	4093
CATTATTTT TTCTACAATC TCCCCTTTAC TTCTCTATT TTCTCTTTCT GGACCTCCCA	4153
TTATTAGAC CTCTTTCCTC TAGTTTTATT GTCTCTTCTA TTTCCCATCT CTTTGACTTT	4213
GTGTTTTCTT TCAGGGAAGT TTCTTTTTTT TCTTTTTTTT TGAGATGGAG TTCACTCTT	4273
GTGTGCCAG GCTGGAGTGC AATGACGTGA TCTCAGCTCA CCACAACCTC CGCTCCTGG	4333
ATTCAAGCGA TTCTCCTGCC GCAGCCTCCC GAGTAGCTGG GATTACAGGC ATGCGCCACC	4393
ACGCCCAGCT AATTTTGTGT TTTTAGTAGA GAAGGGGTTT CTCCGTGTTG GTCAAGCTGG	4453

FIG. 2D

CTG GCC TGC GGG GCA GTG CTC ATC CAC CCC TCC TGG GTG CTG ACA GCG 7213
Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr Ala

GCC CAC TGC ATG GAT GAG TCC AAG AAG CTC CTT GTC AGG CTT 7255
Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu
223

GGTATGGGCT GGAGCCAGGC AGAAGGGGGC TGCCAGAGGC CTGGGTAGGG GGACCAGGCA 7315

GGCTGTTGAG GTTTGGGGGA CCCCCTCC CAGGTGCTTA AGCAAGAGGC TTCTTGAGCT 7375

CCACAGAAAGG TGTGTTGGGGG GAAGAGGCCT ATGTGCCCCC ACCCTGCCCCA CCCATGTACA 7435

CCCAGTATTT TGCAGTAGGG GGTCTCTGG TGCCCTCTTC GAATCTGGGC ACAGGTACCT 7495

GCACACACAT GTTTGTGAGG GGCTACACAG ACCTTCACCT CTCCACTCCC ACTCATGAGG 7555

AGCAGGCTGT GTGGGCCTCA GCACCCCTGG GTGCAGAGAC CAGCAAGGCC TGGCCTCAGG 7615

GCTGTGCCTC CCACAGACTG ACAGGGATGG AGCTGTACAG AGGGAGCCCT AGCATCTGCC 7675

AAAGCCACAA GCTGCTTCCC TAGCAGGCTG GGGGCTCCTA TGCATTGGCC CCGATCTATG 7735

GCAATTTCTG GAGGGGGGGT CTGGCTCAAC TCTTCTGCC AAAAGAAGG CAAAGCATAT 7795

TGAGAAAGGC CAAATTCACA TTTCTACAG CATAATCTAT GCCAGTGCC CCGTGGGGCT 7855

TGGCTTAGAA TTCCAGGTG CTCTTCCAG GGAACCATCA GTCTGGACTG AGAGGACCTT 7915

CTCTCTCAGG TGGGACCCGG CCCTGTCTC CCTGGCAGTG CCGTGTCTG GGGGTCTCC 7975

TCTCTGGGTC TACTGCCCC TGGGGTCTCT CCAGCTACCT TTGCTCCATG TTCCTTTGTG 8035

GCTCTGGTCT GTGTCTGGGG TTTCCAGGGG TCTCGGGCTT CCCTGCTGCC CATTCTTCT 8095

CTGGTCTCAC GGCTCCGTGA CTCCTGAAAA CCAACCAGCA TCCTACCCCT TTGGATTGAC 8155

ACCTGTTGGC CACTCCTTCT GGCAGGAAAA GTCACCGTTG ATAGGGTTCC ACGGCATAGA 8215

CAGGTGGCTC CGCGCCAGTG CCTGGGACGT GTGGGTGCAC AGTCTCCGGG TGAACCTTCT 8275

TCAGGCCCTC TCCAGGCCT GCAGGGGCAC ACCAGTGGGT GGGCCTCAGG AAAGTGCCAC 8335

TGGGGAGAGG CTCCCCGCAG CCCACTCTGA CTGTGCCCTC TGCCCTGCA GGA GAG 8390
Gly Glu
224

TAT GAC CTG CGG CGC TGG GAG AAG TGG GAG CTG GAC CTG GAC ATC AAG 8438
Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys

FIG. 2G

	CGG CGA ACT	-42
TGG AGT ATC TCC ACG ACC CCC CCC TGT GCC AGT CCC TCC AGA ATG TGG	Met Trp	6
	-42	
CAG CTC ACA AGC CTC CTG CTG TTC GTG GCC ACC TGG GGA ATT TCC GGC		54
Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile Ser Gly		
	-40	
	-30	
ACA CCA GCT CCT CTT GAC TCA GTG TTC TCC AGC AGC GAG CGT GCC CAC		102
Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg Ala His		
	-20	
	-10	
CAG GTG CTG CGG ATC CGC AAA CGT GCC AAC TCC TTC CTG GAG GAG CTC		150
Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu Glu Leu		
	-1 +1	
CGT CAC AGC AGC CTG GAG CGG GAG TGC ATA GAG GAG ATC TGT GAC TTC		198
Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys Asp Phe		
	10 20	
GAG GAG GCC AAG GAA ATT TTC CAA AAT GTG GAT GAC ACA CTG GCC TTC		246
Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu Ala Phe		
	30 40	
TGG TCC AAG CAC GTC GAC GGT GAC CAG TGC TTG GTC TTG CCC TTG GAG		294
Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro Leu Glu		
	50	
CAC CCG TGC GCC AGC CTG TGC TGC GGG CAC GGC ACG TGC ATC GAC GGC		342
His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile Asp Gly		
	60 70	
ATC GGC AGC TTC AGC TGC GAC TGC CGC AGC GGC TGG GAG GGC CGC TTC		390
Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly Arg Phe		
	80	
TGC CAG CGC GAG GTG AGC TTC CTC AAT TGC TCT CTG GAC AAC GGC GGC		438
Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn Gly Gly		
	90 100	
TGC ACG CAT TAC TGC CTA GAG GAG GTG GGC TGG CGG CGC TGT AGC TGT		486
Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys Ser Cys		
	110 120	
GCG CCT GGC TAC AAG CTG GGG GAC GAC CTC CTG CAG TGT CAC CCC GCA		534
Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His Pro Ala		
	130	
GTG AAG TTC CCT TGT GGG AGG CCC TGG AAG CGG ATG GAG AAG AAG CGC		582
Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys Lys Arg		
	140 150	

FIG. 3A

AGT CAC CTG AAA CGA GAC ACA GAA GAC CAA GAA GAC CAA GTA GAT CCG 630
Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val Asp Pro
160

CGG CTC ATT GAT GGG AAG ATG ACC AGG CGG GGA GAC AGC CCC TGG CAG 678
Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro Trp Gln
170 180

GTG GTC CTG CTG GAC TCA AAG AAG AAG CTG GCC TGC GGG GCA GTG CTC 726
Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala Val Leu
190 200

ATC CAC CCC TCC TGG GTG CTG ACA GCG GCC CAC TGC ATG GAC GAG TCC 774
Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp Glu Ser
210

AAG AAG CTC CTT GTC AGG CTT GGA GAG TAT GAC CTG CGG CGC TGG GAG 822
Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg Trp Glu
220 230

AAG TGG GAG CTG GAC CTG GAC ATC AAG GAG GTC TTC GTC CAC CCC AAC 870
Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His Pro Asn
240

TAC AGC AAG AGC ACC ACC GAC AAT GAC ATC GCA CTG CTG CAC CTG GCC 918
Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His Leu Ala
250 260

CAG CCC GCC ACC CTC TCG CAG ACC ATA GTG CCC ATC TGC CTC CCG GAC 966
Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu Pro Asp
270 280

AGC GGC CTT GCA GAG CGC GAG CTC AAT CAG GCC GGC CAG GAG ACC CTC 1014
Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu Thr Leu
290

GTG ACG GGC TGG GGC TAC CAC AGC AGC CGA GAG AAG GAG GCC AAG AGA 1062
Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala Lys Arg
300 310

AAC CGC ACC TTC GTC CTC AAC TTC ATC AAG ATT CCC GTG GTC CCG CAC 1110
Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val Pro His
320

AAT GAG TGC AGC GAG GTC ATG AGC AAC ATG GTG TCT GAG AAC ATG CTG 1158
Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn Met Leu
330 340

TGT GCG GGC ATC CTC GGG GAC CGG CAG GAT GCC TGC GAG GGC GAC AGT 1206
Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly Asp Ser
350 360

GGG GGG CCC ATG GTC GCC TCC TTC CAC GGC ACC TGG TTC CTG GTG GGC 1254
Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu Val Gly
370

FIG. 3B